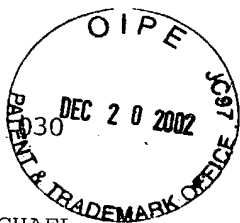


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ARAND et al  
Serial No.: 10/009,030



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78

<110> ARAND, MICHAEL  
ARCHELAS, ALAIN ROBERT  
BARATI, JACQUES  
FURSTOSS, ROLAND

<120> EPOXIDE HYDROLASES OF ASPERGILLUS ORIGIN

<130> bml-410.018

<140> 10/009,030

<141> 2001-11-02

<150> PCT/FR00/01217

<151> 2000-05-05

<150> FR 99/05711

<151> 1999-05-05

<160> 8

<170> PatentIn Ver. 2.1

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<211> 1197

<212> DNA

<213> Aspergillus niger

<220>

<221> CDS

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aat cct ttc acg gtc tct atc ccg gat gaa cag ttg gat gac ttg aaa	96
Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gln Leu Asp Asp Leu Lys	
20 25 30	

acc ctc gtc cga ctg tcc aag att gct cct ccc acc tat gag agc ctg	144
Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu	
35 40 45	

caa gcg gat ggc cgg ttt ggc atc act tct gaa tgg ctg aca act atg	192
Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met	
50 55 60	

cgg gag aaa tgg ctc tcg gag ttt gac tgg cga cca ttt gaa gct cga	240
Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg	
65 70 75 80	

ctg aac tct ttc cct cag ttt act aca gag atc gag ggt ctc acg att	288
Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile	
85 90 95	

cac ttt gct gct ctc ttc tcc gag agg gag gat gct gtg cct atc gca	336
His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala	
100 105 110	
ttg ctc cat ggt tgg ccc ggc agc ttc gtt gag ttc tac cca atc ctg	384
Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu	
115 120 125	
cag cta ttc cgg gag gag tac acc cct gag act ctg cca ttc cat ctg	432
Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu	
130 135 140	
gtt gtt ccg tcc ctt cct ggg tat act ttt tca tct ggt ccc ccg ctg	480
Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu	
145 150 155 160	
gac aag gac ttc ggc ttg atg gac aac gcc cgg gtc gta gac cag ttg	528
Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu	
165 170 175	
atg aag gac ctc ggg ttc gga agt ggt tat att att cag gga ggt gat	576
Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp	
180 185 190	
att ggt agc ttt gtt gga cga ctg ttg ggc gtg ggt ttc gac gcc tgc	624
Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys	
195 200 205	
aaa gcg gtt cat ttg aac ctg tgc gca atg agg gct ccc cct gag ggc	672
Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly	
210 215 220	
ccg tca att gag agc ttg tcc gca gcg gag aag gag gga atc gcg cga	720
Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg	
225 230 235 240	
atg gag aag ttc atg acc gat ggc tta gct tat gcc atg gag cac agt	768
Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser	
245 250 255	
act cgg ccc agt act att ggc cac gtg ctg tcc agc agt ccg atc gca	816
Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala	
260 265 270	
tta ctt gca tgg att ggt gag aaa tat ctc caa tgg gtg gat aaa ccc	864
Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro	
275 280 285	
ctc cct tct gag acc atc ctc gag atg gtg agc ctg tat tgg ctg acg	912
Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr	
290 295 300	
gaa agt ttc ccg cgg gca att cat acc tac cgc gag act acc cca act	960
Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr	
305 310 315 320	

gcc tcc gct ccc aat gga gcg aca atg ctt cag aag gaa tta tat att 1008  
 Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile  
                   325                                  330                                  335

cac aag ccg ttt ggg ttc tcc ttc ttc ccc aag gac ctt tgt cct gtg 1056  
 His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val  
                   340                                  345                                  350

cct cgg agc tgg att gct aca acg gga aat cta gta ttc ttc cgg gat 1104  
 Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp  
                   355                                  360                                  365

cat gca gag gga gga cac ttt gcc gca ttg gag cgt cca cgc gag ctg 1152  
 His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu  
                   370                                  375                                  380

aag acc gac ctg aca gca ttt gtc gag cag gtg tgg cag aag tag 1197  
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<212> PRT

<213> Aspergillus niger

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                   20                                  25                                  30

Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu  
                   35                                  40                                  45

Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met  
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Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg  
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Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile  
                   85                                  90                                  95

His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala  
                   100                                  105                                  110

Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu  
                   115                                  120                                  125

Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu  
                   130                                  135                                  140

Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu  
                   145                                  150                                  155                                  160

Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu  
 165 170 175  
 Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp  
 180 185 190  
 Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys  
 195 200 205  
 Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly  
 210 215 220  
 Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg  
 225 230 235 240  
 Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser  
 245 250 255  
 Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala  
 260 265 270  
 Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro  
 275 280 285  
 Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr  
 290 295 300  
 Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr  
 305 310 315 320  
 Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile  
 325 330 335  
 His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val  
 340 345 350  
 Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp  
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 His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu  
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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cgcgggcaat ccacacctac 20

<210> 5  
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<212> DNA  
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<223> Description of Artificial Sequence: Primer

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<210> 6  
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<212> DNA  
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<223> Description of Artificial Sequence: Primer

<400> 6  
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<210> 7  
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<223> Description of Artificial Sequence: Primer

<400> 7  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

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44

## SEQUENCE LISTING

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5 <120> PROTEINS OF FUNGAL ORIGIN AND DERIVATIVES,  
 PROCESSES FOR OBTAINING THEM, AND THEIR USES, IN  
 PARTICULAR FOR THE PREPARATION OF ENANTIOMERICALLY  
 PURE MOLECULES

10 &lt;130&gt; EPOXSL

&lt;140&gt;

&lt;141&gt;

15 &lt;160&gt; 2

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

20 &lt;211&gt; 1197

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

&lt;220&gt;

25 &lt;221&gt; CDS

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Nucleotide sequence SEQ ID NO : 1

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35 aat cct ttc acg gtc tct atc ccg gat gaa cag ttg gat gac ttg aaa 96  
 Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gln Leu Asp Asp Leu Lys  
 20 25 30

40 acc ctg gtc cga ctg tcc aag att gct cct ccc acc tat gag agc ctg 144  
 Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu  
 35 40 45

45 caa gcg gat ggc cgg ttt ggc atc act tct gaa tgg ctg aca act atg 192  
 Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met  
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50 cgg gag aaa tgg ctg tcg gag ttt gac tgg cga cca ttt gaa gct cga 240  
 Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg  
 65 70 75 80

50 ctg aac tct ttc cct cag ttt act aca gag atc gag ggt ctg acg att 288  
 Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile  
 85 90 95

55 cac ttt gct gct ctg ttc tcc gag agg gag gat gct gtg cct atc gca 336  
 His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala  
 100 105 110

60 ttg ctg cat ggt tgg ccc ggc agc ttc gtt gag ttc tac cca atc ctg 384  
 Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu  
 115 120 125

5	cag cta ttc cgg gag gag tac acc cct gag act ctg cca ttc cat ctg Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu 130 135 140	432
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15	gac aag gac ttc ggc ttg atg gac aac gcc cgg gtc gta gac cag ttg Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu 165 170 175	528
20	atg aag gac ctc ggg ttc gga agt ggt tat att att cag gga ggt gat Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp 180 185 190	576
25	att ggt agc ttt gtt gga cga ctg ttg ggc gtg ggt ttc gac gcc tgc Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys 195 200 205	624
30	aaa gcg gtt cat ttg aac ctg tgc gca atg agg gct ccc cct gag ggc Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly 210 215 220	672
35	ccg tca att gag agc ttg tcc gca gcg gag aag gag gga atc gcg cga Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg 225 230 235 240	720
40	atg gag aag ttc atg acc gat ggc tta gct tat gcc atg gag cac agt Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser 245 250 255	768
45	act cgg ccc agt act att ggc cac gtg ctg tcc agc agt ccg atc gca Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala 260 265 270	816
50	tta ctt gca tgg att ggt gag aaa tat ctc caa tgg gtg gat aaa ccc Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro 275 280 285	864
55	ctc cct tct gag acc atc ctc gag atg gtg agc ctg tat tgg ctg acg Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr 290 295 300	912
60	gaa agt ttc ccg cgg gca att cat acc tac cgc gag act acc cca act Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr 305 310 315 320	960
65	gcc tcc gct ccc aat gga gcg aca atg ctt cag aag gaa tta tat att Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile 325 330 335	1008
70	cac aag ccg ttt ggg ttc tcc ttc ttc ccc aag gac ctt tgt cct gtg His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val 340 345 350	1056
75	cct cgg agc tgg att gct aca acg gga aat cta gta ttc ttc cgg gat Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp 355 360 365	1104



cat gca gag gga gga cac ttt gcc gca ttg gag cgt cca cgc gag ctg 1152  
 His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu  
 370 375 380

5 aag acc gac ctg aca gca ttt gtc gag cag gtg tgg cag aag tag 1197  
 Lys Thr Asp Leu Thr Ala Phe Val Glu Gln Val Trp Gln Lys  
 385 390 395

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20 Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gln Leu Asp Asp Leu Lys  
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Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu  
 35 40 45

25 Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met  
 50 55 60

30 Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg  
 65 70 75 80

Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile  
 85 90 95

35 His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala  
 100 105 110

Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu  
 115 120 125

40 Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu  
 130 135 140

45 Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu  
 145 150 155 160

Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu  
 165 170 175

50 Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp  
 180 185 190

Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys  
 195 200 205

55 Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly  
 210 215 220

60 Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg  
 225 230 235 240

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	Leu	Leu	Ala	Trp	Ile	Gly	Glu	Lys	Tyr	Leu	Gln	Trp	Val	Asp	Lys	Pro	
			275					280					285				
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		290					295					300					
	Glu	Ser	Phe	Pro	Arg	Ala	Ile	His	Thr	Tyr	Arg	Glu	Thr	Thr	Pro	Thr	
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	Ala	Ser	Ala	Pro	Asn	Gly	Ala	Thr	Met	Leu	Gln	Lys	Glu	Leu	Tyr	Ile	
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		370					375					380					
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30	385					390					395						